First molecular characterization of Giardia duodenalis from goats in Malaysia

ABSTRACT

In the present study, 310 faecal samples from goats from eight different farms in Malaysia were tested for the presence of Giardia using a PCR-coupled approach. The nested PCR for SSU amplified products of the expected size (∼200 bp) from 21 of 310 (6.8%) samples. Sixteen of these 21 products could be sequenced successfully and represented six distinct sequence types. Phylogenetic analysis of the SSU sequence data using Bayesian Inference (BI) identified Giardia assemblages A, B and E. The identification of the ‘zoonotic’ assemblages A and B suggests that Giardia-infected goats represent a possible reservoir for human giardiasis in Malaysia.

Keyword: Giardia duodenalis; Small subunit of the nuclear ribosomal RNA (SSU) gene; Goats; Malaysia.